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**RAW SEQUENCE LISTING
PATENT APPLICATION US/09/635,864**DATE: 10/05/2000
TIME: 01:46:19*INPUT SET: S35971.raw*

#3

This Raw Listing contains the General
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING
2
3 (1) General Information:
4
5 (i) APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA, MARGHERITA
6
7 (ii) TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS
8
9 (iii) NUMBER OF SEQUENCES: 99
10
11 (iv) CORRESPONDENCE ADDRESS:
12 (A) ADDRESSEE: Klauber & Jackson
13 (B) STREET: 411 Hackensack Avenue
14 (C) CITY: Hackensack
15 (D) STATE: New Jersey
16 (E) COUNTRY: USA
17 (F) ZIP: 07601
18
19 (v) COMPUTER READABLE FORM:
20 (A) MEDIUM TYPE: Floppy disk
21 (B) COMPUTER: IBM PC compatible
22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
24
25 (vi) CURRENT APPLICATION DATA:
26 (A) APPLICATION NUMBER: 09/635,864
27 (B) FILING DATE: August 10, 2000
28 (C) CLASSIFICATION:
29
30 (vii) PRIOR APPLICATION DATA:
31 (A) APPLICATION NUMBER: 08/438,431
32 (B) FILING DATE: May 10, 1995
33 (C) CLASSIFICATION:
34
35 (vii) PRIOR APPLICATION DATA:
36 (A) APPLICATION NUMBER: 08/347,563
37 (B) FILING DATE: November 30, 1994
38 (C) CLASSIFICATION:
39
40 (vii) PRIOR APPLICATION DATA:
41 (A) APPLICATION NUMBER: 08/292,345
42 (B) FILING DATE: August 17, 1994
43 (C) CLASSIFICATION:
44
45 (viii) ATTORNEY/AGENT INFORMATION:
46 (A) NAME: Jackson Esq., David A.

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47 (B) REGISTRATION NUMBER: 26,742
48 (C) REFERENCE/DOCKET NUMBER: 600-1-087 CIP1

50 (ix) TELECOMMUNICATION INFORMATION:
51 (A) TELEPHONE: 201 487-5800
52 (B) TELEFAX: 201 343-1684
53 (C) TELEX: 133521

55 (2) INFORMATION FOR SEO ID NO:1:

56
57 (i) SEQUENCE CHARACTERISTICS:
58 (A) LENGTH: 2793 base pairs
59 (B) TYPE: nucleic acid
60 (C) STRANDEDNESS: double
61 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(A) DESCRIPTION: Murine ob cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI SENSE: NO

69
70 (vi) ORIGINAL SOURCE:
71 (A) ORGANIZATION

72

73 (ix) FEATURE:
74 (A) NAME/KEY: CDS
75 (B) LOCATION: 57 560

78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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79 GGATCCCTGC TCCAGCAGCT GCAAGGTGCA AGAAGAAGAA GATCCCAGGG AGGAAA      56
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81
82 ATG TGC TGG AGA CCC CTG TGT CGG TTC CTG TGG CTT TGG TCC TAT CTG    104
83 Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
84   1           5           10          15
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86 TCT TAT GTT CAA GCA GTG CCT ATC CAG AAA GTC CAG GAT GAC ACC AAA    152
87 Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
88   20          25          30
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90 ACC CTC ATC AAG ACC ATT GTC ACC AGG ATC AAT GAC ATT TCA CAC ACG    200
91 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
92   35          40          45
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94 CAG TCG GTA TCC GCC AAG CAG AGG GTC ACT GGC TTG GAC TTC ATT CCT    248
95 Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
96   50          55          60
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98 GGG CTT CAC CCC ATT CTG AGT TTG TCC AAG ATG GAC CAG ACT CTG GCA    296
99 Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala

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102	GTC TAT CAA CAG GTC CTC ACC AGC CTG CCT TCC CAA AAT GTG CTG CAG				344
103	Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln				
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106	ATA GCC AAT GAC CTG GAG AAT CTC CGA GAC CTC CTC CAT CTG CTG GCC				392
107	Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala				
108	100	105	110		
109					
110	TTC TCC AAG AGC TGC TCC CTG CCT CAG ACC AGT GGC CTG CAG AAG CCA				440
111	Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro				
112	115	120	125		
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114	GAG AGC CTG GAT GGC GTC CTG GAA GCC TCA CTC TAC TCC ACA GAG GTG				488
115	Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val				
116	130	135	140		
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118	GTG GCT TTG AGC AGG CTG CAG GGC TCT CTG CAG GAC ATT CTT CAA CAG				536
119	Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln				
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121					
122	TTG GAT GTT AGC CCT GAA TGC TGA AGTTTCAAAG GCCACCAGGC TCCCAAGA				588
123	Leu Asp Val Ser Pro Glu Cys *				
124	165				
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126	ATCATGTAGA GGGAGAAC CTTGGCTTCC AGGGGTCTTC AGGAGAACAG AGCCATGTGC				648
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130	CAATGCTTGA CTCAAGTTAT CCACACAAC TCATGAGCAC AAGGAGGGC CAGCCTGCAG				768
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132	AGGGGACTCT CACCTAGTTC TTCAGCAAGT AGAGATAAGA GCCATCCCAT CCCCTCCATG				828
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134	TCCCACCTGC TCCGGGTACA TGTTCCCTCCG TGGGTACACG CTTCGCTGCG GCCCAGGAGA				888
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136	GGTGAGGTAG GGATGGTAG AGCCTTGGG CTGTCTCAGA GTCTTGGGA GCACCGTGAA				948
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138	GGCTGCATCC ACACACAGCT GGAAACTCCC AAGCAGCACA CGATGGAAGC ACTTATTTAT				1008
139					
140	TTATTCTGCA TTCTATTTG GATGGATCTG AAGCAAGGCA TCAGCTTTTT CAGGCTTGG				1068
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142	GGGTCAGCCA GGATGAGGAA GGCTCCTGGG GTGCTGCTTT CAATCCTATT GATGGGTCTG				1128
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144	CCCGAGGCAA ACCTAATTT TGAGTGACTG GAAGGAAGGT TGGGATCTTC CAAACAAGAG				1188
145					
146	TCTATGCAGG TAGCGCTCAA GATTGACCTC TGGTGACTGG TTTTGTTCT ATTGTGACTG				1248
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148	ACTCTATCCA AACACGTTG CAGCGGCATT GCCGGGAGCA TAGGCTAGGT TATTATCAA				1308
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151					
152	TTAGAGGGAG GGTGAAGGAT CCGGAAGTGT TCTCTGAATT ACATATGTGT GGTAGGCTTT				1428

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153 TCTGAAAGGG TGAGGCATTT TCTTACCTCT GTGCCACAT AGTGTGGCTT TGTGAAAAGG 1488
154 ACAAAGGAGT TGACTCTTC CGGAACATTG GGAGTGTACC AGGCACCCCTT GGAGGGGCTA 1548
155 156 AAGCTACAGG CCTTTGTTG GCATATTGCT GAGCTCAGGG AGTGAGGGCC CCACATTGA 1608
157 158 GACAGTGAGC CCCAAGAAAA GGGTCCCTGG TGTAGATCTC CAAGGTTGTC CAGGGTTGAT' 1668
159 160 CTCACAATGC GTTCTTAAG CAGGTAGACG TTTGCATGCC AATATGTGGT TCTCATCTGA 1728
161 162 TTGGTTCATC CAAAGTAGAA CCCTGTCTCC CACCCATTCT GTGGGGAGTT TTGTTCCAGT 1788
163 164 GGGAAATGAGA AATCACTTAG CAGATGGTCC TGAGCCCTGG GCCAGCACTG CTGAGGAAGT 1848
165 166 GCCAGGGCCC CAGGCCAGGC TGCCAGAATT GCCCTTCGGG CTGGAGGATG AACAAAGGG 1908
167 168 CTTGGGTTTT TCCATCACCC CTGCACCCCTA TGTCACCACAT AAACCTGGGG GCAGATCAGT 1968
169 170 GAGAGGACAC TTGATGGAAA GCAATACACT TTAAGACTGA GCACAGTTTC GTGCTCAGCT 2028
171 172 CTGTCTGGTG CTGTGAGCTA GAGAACGCTA CCACATACAT ATAAAAATCA GAGGCTCATG 2088
173 174 TCCCTGTGGT TAGACCCTAC TCGCGGCGGT GTACTCCACC ACAGCAGCAC CGCACCGCTG 2148
175 176 GAAGTACAGT GCTGTCTTCA ACAGGTGTGA AAGAACCTGA GCTGAGGGTG ACAGTGCCA 2208
177 178 GGGGAACCCCT GCTTGCAGTC TATTGCATTG ACATACCGCA TTTCAGGGCA CATTAGCATC 2268
179 180 CACTCCTATG GTAGCACACT GTTGACAATA GGACAAGGGA TAGGGTTGA CTATCCCTA 2328
181 182 TCCAAAATGC TTGGGACTAG AAGAGTTTG GATTTAGAG TCTTTTCAGG CATAGGTATA 2388
183 184 TTTGAGTATA TATAAAATGA GATATCTTGG GGATGGGCC CAAGTATAAA CATGAAGTTC 2448
185 186 ATTTATATTT CATAATACCG TATAGACACT GCTTGAAGTG TAGTTTTATA CAGTGTTTA 2508
187 188 AATAACGTTG TATGCATGAA AGACGTTTT ACAGCATGAA CCTGTCTACT CATGCCAGCA 2568
189 190 CTCAAAAACC TTGGGTTTT GGAGCAGTTT GGATCTTGGG TTTTCTGTTA AGAGATGGTT 2628
191 192 AGCTTATAACC TAAAACCATA ATGGCAAACA GGCTGCAGGA CCAGACTGGA TCCTCAGCCC 2688
193 194 TGAAGTGTGC CCTTCCAGCC AGGTCATACC CTGTGGAGGT GAGCGGGATC AGGTTTGTG 2748
195 196 197 198 GTGCTAAGAG AGGAGTTGGA GGTAGATTTT GGAGGATCTG AGGGC 2793
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200
201 (2) INFORMATION FOR SEQ ID NO:2:
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203 (i) SEQUENCE CHARACTERISTICS:
204 (A) LENGTH: 167 amino acids
205 (B) TYPE: amino acid

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206 (D) TOPOLOGY: linear
207
208 (ii) MOLECULE TYPE: protein
209 (A) DESCRIPTION: Murine ob polypeptide
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211 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
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213 Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
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215
216 Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
217 20 25 30
218
219 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
220 35 40 45
221
222 Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
223 50 55 60
224
225 Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
226 65 70 75 80
227
228 Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln
229 85 90 95
230
231 Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
232 100 105 110
233
234 Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro
235 115 120 125
236
237 Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val
238 130 135 140
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240 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln
241 145 150 155 160
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243 Leu Asp Val Ser Pro Glu Cys
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247 (2) INFORMATION FOR SEQ ID NO:3:
248
249 (i) SEQUENCE CHARACTERISTICS:
250 (A) LENGTH: 700 base pairs
251 (B) TYPE: nucleic acid
252 (C) STRANDEDNESS: double
253 (D) TOPOLOGY: linear
254
255 (ii) MOLECULE TYPE: cDNA
256 (A) DESCRIPTION: Human ob cDNA where N represents any nucleotide
257
258 (iii) HYPOTHETICAL: NO

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SEQUENCE VERIFICATION REPORT
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